

SeqServer®

biology in silico

BLAST2 Search Results

Sequences Help

Retrieval BLAST2 FASTA ClustalW GCG Assembly Phrap Translation

BLAST2 Manual

Confidential -- Property of Incyte Corporation SeqServer Version 4.6 Jan 2002

Program: **blastp**

Sequence ID(s):

983910CD1 vs. genpept136

NCBI-BLASTP 2.0.10 [Aug-26-1999]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= 983910CD1
(314 letters)

Database: genpept136

1,453,555 sequences; 449,659,834 total letters

Searching.....done

Sequences producing significant alignments:		Score	E
		(bits)	Value
<input checked="" type="checkbox"/>	g3002935 T cell receptor beta chain [Homo sapiens]	550	e-155
<input checked="" type="checkbox"/>	g1100182 T-cell receptor beta [Homo sapiens]	546	e-154
<input checked="" type="checkbox"/>	g339012 T-cell receptor precursor [Homo sapiens]	522	e-147
<input checked="" type="checkbox"/>	g6741519 unnamed protein product (unidentified)	490	e-137
<input checked="" type="checkbox"/>	g29469988 T cell receptor beta chain BV12S1 J1-1 BC1 [Homo sa	490	e-137
>g3002935 T cell receptor beta chain [Homo sapiens]		Length = 309	

Score = 550 bits (1401), Expect = e-155
Identities = 272/311 (87%), Positives = 280/311 (89%), Gaps = 3/311 (0%)
Query: 1 MDTLLWALCLLGADHTGAGVSGTSPKRVTEKGVKVELRCDPISGHTALWYROSQQ 60
Sbjct: 1 MDTLLWAFCLLGADHTGAGVSGTSPKRVTEKGVKVELRCDPISGHTALWYROSQQ 60

Query: 61 GFEELTYFGTGAADSGLRNDFPVRPESVSTLKIQRTQEDSAAYLRAGVAGMS 120
G EFLITFG A D SGLPDRF A R GSVETL IRTQ Q DSA YL A + S
Sbjct: 61 GLEELTYFGNAPKSGLPDRFSAERTGSGVSTLTQRTQEDSAVIL--CASSLSL 117
Query: 121 VNEQYFGTRULVLELKNFPEFVAVFEPSEAEISHTOKATLVCLATGFYDVELSW 180
+ +FC GTRULV EDL VFFEFVAVFEPSEAEISHTOKATLVCLATG +FDVELSW
Sbjct: 118 LSPLEFGTRULVTEDEAKVFPPEVAVFEPSEAEISHTOKATLVCLATGFYDVELSW 177
Query: 181 WNGKEVHSGVSTDQPLKEQPALANDSRVCLSSRLRVSAATPMQNFNFRCCQVQYGLSE 240
W NKGKHSVSTDQPLKEQPALANDSRVCLSSRLRVSAATPMQNFNFRCCQVQYGLSE 237
Sbjct: 178 WNGKEVHSGVSTDQPLKEQPALANDSRVCLSSRLRVSAATPMQNFNFRCCQVQYGLSE 237
Query: 241 NDEMTQRAKPVTVQVNSADWAGRADCGFTSSTQGVLSATILYELLGKATLVAVLSA 300
NDEMTQRAKPVTVQVNSADWAGRADCGFTS STQGVLSATILYELLGKATLVAVLSA
Sbjct: 238 NDEMTQRAKPVTVQVNSADWAGRADCGFTSSTQGVLSATILYELLGKATLVAVLSA 297
Query: 301 LVLMAMVKKDSRG 314
LVLMAMVKKDSRG
Sbjct: 298 LVLMAMVKKDSRG 308

>g1100182 T-cell receptor beta [Homo sapiens]
Length = 311

Score = 546 bits (1391), Expect = e-154
Identities = 268/314 (85%), Positives = 282/314 (89%), Gaps = 3/314 (0%)
Query: 1 MDTLLWALCLLGADHTGAGVSGTSPKRVTEKGVKVELRCDPISGHTALWYROSQQ 60
MGT LLGW ALCLLGADH GVSQ P +K+T++G++V RCDPIS H LWWYRQ-LQQ 60
Sbjct: 1 MDTLLWALCLLGADHTGAGVSGTSPKRVTEKGVKVELRCDPISGHTALWYROSQQ 60

Query: 61 GFEELTYFGTGAADSGLRNDFPVRPESVSTLKIQRTQEDSAAYLRAGVAGMS 120
GFEEL YFG + S L +DRF A RP+GS STL+IQRTQEDSA YL A ++ +S
Sbjct: 61 GFEELTYFONEAQLKSRLLSDRFSAERPKGSPFTLEIQRTQEDSAWYLCA--SSNGTS 118

Query: 121 VNEQYFGTRULVLELKNFPEFVAVFEPSEAEISHTOKATLVCLATGFYDVELSW 180
Y EQYFGTRULV EDLKNFPEFVAVFEPSEAEISHTOKATLVCLATGFYDVELSW
Sbjct: 119 Y-EQYFGTRULVTEDEAKVFPPEVAVFEPSEAEISHTOKATLVCLATGFYDVELSW 177

Query: 181 WNGKEVHSGVSTDQPLKEQPALANDSRVCLSSRLRVSAATPMQNFNFRCCQVQYGLSE 240
W NKGKHSVSTDQPLKEQPALANDSRVCLSSRLRVSAATPMQNFNFRCCQVQYGLSE 237
Sbjct: 178 WNGKEVHSGVSTDQPLKEQPALANDSRVCLSSRLRVSAATPMQNFNFRCCQVQYGLSE 237

Query: 241 NDEMTQRAKPVTVQVNSADWAGRADCGFTSSTQGVLSATILYELLGKATLVAVLSA 300
NDEMTQRAKPVTVQVNSADWAGRADCGFTSSTQGVLSATILYELLGKATLVAVLSA
Sbjct: 238 NDEMTQRAKPVTVQVNSADWAGRADCGFTSSTQGVLSATILYELLGKATLVAVLSA 297

Query: 301 LVLMAMVKKDSRG 314
LVLMAMVKKDSRG
Sbjct: 298 LVLMAMVKKDSRG 311

>g339012 T-cell receptor precursor [Homo sapiens]
Length = 310

Score = 522 bits (1330), Expect = e-147
Identities = 254/311 (81%), Positives = 271/311 (86%), Gaps = 2/311 (0%)

BLAST2 Results

http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer

BLAST2 Results

http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer

Query: 1 MGTLLQWALCALCAGDHGTGAGVSGTFSNNKVTKEGVDVELRCDPISGHTALWYRQSLQ 60
MGT LLQW ALCLGADH GVSQ P + *T+G+V RCDPIS H LWMRQ+LQ 60
Sbjct: 1 MGTSLQWALCALCAGDHADTGVSNFRNITKROQNTFRCDPISGHNELWYRQTLQ 60
Query: 61 GPEELTYQGAADSGGLNDRFPFVRPESVSTLKIQTEQDSAAVLRAGVAGNSS 120
GPEEL YQ + S L +DRF A R+GS STL+IQTEQDSA YL A AG +
Sbjct: 61 GPEELTYQEAQLSKRLSDFSAERPKGSFSTLEIQTEQDSAMYLCASSLAGLQ 120
Query: 121 YNEQYFGGTRLVLELANKVPFPEAVFEPSEAEISHTOKATVCLATGCFYDRIVELSW 180
Q+FG GTRLV+LEL VFPPEAVFEPSEAEISHTOKATVCLATG +FDRIVELSW
Sbjct: 121 --PQIFGGTRLVLELANKVPFPEAVFEPSEAEISHTOKATVCLATGCFYDRIVELSW 178
Query: 181 WNKKEVHSGVSTDPQLKQPALANDSRVCLSSRLKRVSAFWQNNHFRQCVQYGLSE 240
WNKKEVHSGVSTDPQLKQPALANDSRVCLSSRLKRVSAFWQNNHFRQCVQYGLSE
Sbjct: 179 WNKKEVHSGVSTDPQLKQPALANDSRVCLSSRLKRVSAFWQNNHFRQCVQYGLSE 238
Query: 241 NDEMTQDRAKFTVQVISAENWGRADCGFTS YQGGVLSATLYELLGKATVAVLNSA 300
NDEMTQDRAKFTVQVISAENWGRADCGFTS YQGGVLSATLYELLGKATVAVLNSA
Sbjct: 239 NDEMTQDRAKFTVQVISAENWGRADCGFTS YQGGVLSATLYELLGKATVAVLNSA 298
Query: 301 LVJAMVVRKRD 311
LVJAMVVRKRD
Sbjct: 299 LVJAMVVRKRD 309
>6741519 unnamed protein product [unidentified]
Length = 311

Score = 490 bits (1249), Expect = e-137
Identities = 248/314 (78%), Positives = 267/314 (84%), Gaps = 3/314 (0%)
Query: 1 MGTLLQWALCALCAGDHGTGAGVSGTFSNNKVTKEGVDVELRCDPISGHTALWYRQSLQ 60
M T L-QWA LL A T V+QTPS++VT+ G+V LRC PIS H WYRQ LQ 60
Sbjct: 1 MDTVLQWALFSLKAGLTFEPTVQTSHQVQWQEVILRCVPSINHLVFWYRQLQ 60
Query: 61 GPEELTYQGAADSGGLNDRFPFVRPESVSTLKIQTEQDSAAVLRAGVAGNSS 120
EPL+ F ++ S + +d+f RE+GS TLKI+ T+ DSA Y A ++ +S
Sbjct: 61 KVEPLVSNFNEISEKSEIFDQFSEVERPQSNFTLKISTKLSDSANITCA--SSSTNS 118
Query: 121 YNEQYFGGTRLVLELANKVPFPEAVFEPSEAEISHTOKATVCLATGCFYDRIVELSW 180
Y EQYFGGTRLV EDLKNVPFPEAVFEPSEAEISHTOKATVCLATGCFYDRIVELSW
Sbjct: 119 Y-EQYFGGTRLVLELANKVPFPEAVFEPSEAEISHTOKATVCLATGCFYDRIVELSW 177
Query: 181 WNKKEVHSGVSTDPQLKQPALANDSRVCLSSRLKRVSAFWQNNHFRQCVQYGLSE 240
WNKKEVHSGVSTDPQLKQPALANDSRVCLSSRLKRVSAFWQNNHFRQCVQYGLSE
Sbjct: 178 WNKKEVHSGVSTDPQLKQPALANDSRVCLSSRLKRVSAFWQNNHFRQCVQYGLSE 237
Query: 241 NDEMTQDRAKFTVQVISAENWGRADCGFTS YQGGVLSATLYELLGKATVAVLNSA 300
NDEMTQDRAKFTVQVISAENWGRADCGFTS YQGGVLSATLYELLGKATVAVLNSA
Sbjct: 238 NDEMTQDRAKFTVQVISAENWGRADCGFTS YQGGVLSATLYELLGKATVAVLNSA 297
Query: 301 LVJAMVVRKRD 314
LVJAMVVRKRD
Sbjct: 298 LVJAMVVRKRD 311

>29469988 T cell receptor beta chain BV12s1 J1-1 BC1 [Homo sapiens]
Length = 309

Score = 490 bits (1249), Expect = e-137
Identities = 241/311 (77%), Positives = 262/311 (83%), Gaps = 3/311 (0%)
Query: 1 MGTLLQWALCALCAGDHGTGAGVSGTFSNNKVTKEGVDVELRCDPISGHTALWYRQSLQ 60
M + C +LC+L A HT AGV Q+P ++VTE G+V LRC PISGH -L+WYRQ++ +
Sbjct: 1 MDSMTCCVCSLCIIVAHHTDAGVQISRUHEVTEMQEVLTKCKPISGHSLSLFWYRQWNR 60
Query: 61 GPEELTYQGAADSGGLNDRFPFVRPESVSTLKIQTEQDSAAVLRAGVAGNSS 120
G E LTF DSG+P DRP A P S STLKIQ +E DSA Y A+ ++
Sbjct: 61 GLELLTYNNPFIIDSGHEDRFSAHNPASFTLKIQSEFDSNAVTF--CASSFNG 117
Query: 121 YNEQYFGGTRLVLELANKVPFPEAVFEPSEAEISHTOKATVCLATGCFYDRIVELSW 180
E +FG GTRLV+EDL VFPPEAVFEPSEAEISHTOKATVCLATG+FDRIVELSW
Sbjct: 118 AGEAFFGQTRLVTVEDIANVFPPEAVFEPSEAEISHTOKATVCLATGCFYDRIVELSW 177
Query: 181 WNKKEVHSGVSTDPQLKQPALANDSRVCLSSRLKRVSAFWQNNHFRQCVQYGLSE 240
WNKKEVHSGVSTDPQLKQPALANDSRVCLSSRLKRVSAFWQNNHFRQCVQYGLSE
Sbjct: 178 WNKKEVHSGVSTDPQLKQPALANDSRVCLSSRLKRVSAFWQNNHFRQCVQYGLSE 237
Query: 241 NDEMTQDRAKFTVQVISAENWGRADCGFTS YQGGVLSATLYELLGKATVAVLNSA 300
NDEMTQDRAKFTVQVISAENWGRADCGFTS YQGGVLSATLYELLGKATVAVLNSA
Sbjct: 238 NDEMTQDRAKFTVQVISAENWGRADCGFTS YQGGVLSATLYELLGKATVAVLNSA 297
Query: 301 LVJAMVVRKRD 311
LVJAMVVRKRD
Sbjct: 298 LVJAMVVRKRD 308

Database: genpept136
Posted date: Jul 31, 2003 9:27 AM
Number of letters in database: 449,659,834
Number of sequences in database: 1,453,555

Lambda K H 0.318 0.133 0.411
Gapped
Lambda K H 0.270 0.0470 0.230

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 297167763
Number of Sequences: 1453555
Number of extensions: 12787980
Number of successful extensions: 59096
Number of sequences better than 10.0: 17425
Number of HSP's better than 10.0 without gapping: 4379
Number of HSP's successfully gapped in prelim test: 13046
Number of HSP's that attempted gapping in prelim test: 48416
Number of HSP's gapped (non-prelim): 19060
Length of query: 314
Length of database: 449,659,834
effective HSP length: 56
effective length of query: 258
effective length of database: 368,260,754
effective search space: 95011274532
effective search space used: 95011274532

BLAST2 Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

T: 11
A: 40
X1: 16 (7.3 bits)
X2: 38 (14.8 bits)
X3: 64 (24.9 bits)
S1: 41 (21.7 bits)

Submit sequences to:

